CLAIMS

I claim:

1. A method of improving the expression in a plant of a foreign protein comprising the steps of:

(a) analyzing the pattern of nucleotide codon usage in native plant genes having relatively high levels of expression in plants to select from among the codons coding for the same amino acid the codons for each amino acid which are utilized preferentially by the native plant genes;

(b) synthesizing a chimeric nucleotide coding sequence coding for the expression of the amino acid sequence of the foreign protein with the chimeric coding sequence comprising codons differing from those in the coding sequence in the native organism of the protein and selected from among the codons determined to be preferentially utilized by the native plant genes;

(c) joining the chimeric nucleotide coding sequence with flanking regulatory sequences effective to express the chimeric coding sequence in plants; and

(d) transforming the chimeric coding sequence together with the regulatory sequences into the germ line of the plant so that the foreign protein is efficiently produced in cells of the transformed plant.

2. A method as claimed in Claim 1 wherein the synthesized chimeric nucleotide coding sequence is constructed by the synthesis of oligonucleotide segments which are joined together by complementary sticky ends.

3. A method as claimed in Claim 1 wherein the synthesized chimeric nucleotide coding region is constructed by the steps of synthesizing pairs of overlapping complementary oligonucleotides of opposing strands, hybridizing the respective pairs of oligonucleotides together, extending the strands on the hybridized double stranded nucleotide strand, digesting the ends of the double stranded nucleotide strands to create complementary sticky ends, and joining the complementary sticky ends together to make a single double stranded nucleotide.

4. A method as claimed in Claim 1 wherein the chimeric nucleotide coding sequence is synthesized for a 5' end of the coding region and the chimeric coding region is then joined to a 3' portion of the native coding region for the foreign protein.

5. A method as claimed in Claim 4 wherein the 5' end of the coding region is about 25 codons in length.

6. A method as claimed in Claim 1 wherein the foreign protein is the delta endotoxin crystal protein from Bacillus thuringiensis.

7. A method as claimed in Claim 1 wherein the codons determined to be preferentially expressed in plants disproportionately those codons which have a C or a G nucleotide in the third position in the codon in preference to an A or a T.

8. A method as claimed in Claim 1 wherein the foreign protein is native to a procaryotic organism.

9. A transgenic plant comprising in its genome a chimeric gene coding for the expression of a foreign protein natively produced in a foreign organism, the gene having been inserted into the germ line of the plant by genetic engineering, the coding sequence of the gene differing from the coding sequence of the gene for the protein in its native organism by the substitution of nucleotide codons not preferentially expressed by native plants genes with codons which are preferentially expressed efficiently by native plant genes.

10. A transgenic plant as claimed in Claim 9 wherein the coding sequence of the chimeric gene differs from the coding sequence of the foreign gene sequence in a segment at the 5' end of the coding region.

11. A transgenic plant as claimed in Claim 10 wherein the segment at the 5' end is about 25 codons in length.

12. A transgenic plant as claimed in Claim 9 wherein the coding sequence of the chimeric gene differs from the coding sequence of the procaryotic gene sequence by a larger proportion of C and G nucleotides and a corresponding lesser proportion of A and T nucleotides.

13. A transgenic plant as claimed in Claim 9 wherein the foreign organism is a procaryotic organism.

14. A transgenic plant as claimed in Claim 9 wherein the foreign protein is the delta endotoxin crystal protein from Bacillus thuringiensis.

15. A transgenic plant comprising in its genome a gene coding for the amino-terminal portion of the delta-endotoxin gene of Bacillus thuringiensis, the gene including appropriate regulatory sequences effective in plant cells to express the coding region so that cells of the plant produce the delta-endotoxin protein, the coding sequence of the gene including a 5' region of at least 150 nucleotides in length constructed as an oligonucleotide from nucleotide codons selected from those codons determined to be efficiently expressed in the cells of plants, the sequence of and pattern of codons being different from those in the coding region of the gene in Bacillus thuringiensis.

16. A transgenic plant as claimed in Claim 15 wherein the codons determined to be efficiently expressed in the cells of plants include those codons which have a C or a G in the third position in the codon in preference to those codons which have an A or a T in that position.